

SEQUENCE LISTING



RECEIVED

FEB 07 2000

(1) GENERAL INFORMATION:

(i) APPLICANT: Svendsen, Allan
Bisgård-Frantzen, Henrik
Borchert, Torben Vedel

(ii) TITLE OF INVENTION: α -Amylase Mutants

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Novo Nordisk of North America, Inc.
(B) STREET: 405 Lexington Avenue, 64th Floor
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States of America
(F) ZIP: 10174-6401

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

CS (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/683,838
(B) FILING DATE: 18-JUL-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Green, Reza
(B) REGISTRATION NUMBER: 38,475
(C) REFERENCE/DOCKET NUMBER: 4394.400-US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-867-0123
(B) TELEFAX: 212-878-9655

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1920 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 334..1869

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 334..420

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 421..1869

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAAGATTG GAAGTACAAA AATAAGCAAA AGATTGTCAA TCATGTCATG AGCCATGCGG

60

GAGACGGAAA AATCGTCTTA ATGCACGATA TTTATGCAAC GTTCGCAGAT GCTGCTGAAG	120
AGATTATTAA AAAGCTGAAA GCAAAAAGGCT ATCAATTGGT AACTGTATCT CAGCTTGAAG	180
AAGTGAAGAA GCAGAGAGGC TATTGAATAA ATGAGTAGAA GCGCCATATC GGCGCTTTTC	240
TTTTGGAAGA AAATATAGGG AAAATGGTAC TTGTTAAAAA TTCGGAATAT TTATACAACA	300
TCATATGTTT CACATTGAAA GGGGAGGAGA ATC ATG AAA CAA CAA AAA CGG CTT	354
Met Lys Gln Gln Lys Arg Leu	
-29 -25	
TAC GCC CGA TTG CTG ACG CTG TTA TTT GCG CTC ATC TTC TTG CTG CCT	402
Tyr Ala Arg Leu Leu Thr Leu Phe Ala Leu Ile Phe Leu Leu Pro	
-20 -15 -10	
CAT TCT GCA GCA GCG GCG GCA AAT CTT AAT GGG ACG CTG ATG CAG TAT	450
His Ser Ala Ala Ala Ala Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr	
-5 1 5 10	
TTT GAA TGG TAC ATG CCC AAT GAC GGC CAA CAT TGG AGG CGT TTG CAA	498
Phe Glu Trp Tyr Met Pro Asn Asp Gly Gln His Trp Arg Arg Leu Gln	
15 20 25	
AAC GAC TCG GCA TAT TTG GCT GAA CAC GGT ATT ACT GCC GTC TGG ATT	546
Asn Asp Ser Ala Tyr Leu Ala Glu His Gly Ile Thr Ala Val Trp Ile	
30 35 40	
CCC CCG GCA TAT AAG GGA ACG AGC CAA GCG GAT GTG GGC TAC GGT GCT	594
Pro Pro Ala Tyr Lys Gly Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala	
45 50 55	
TAC GAC CTT TAT GAT TTA GGG GAG TTT CAT CAA AAA GGG ACG GTT CGG	642
Tyr Asp Leu Tyr Asp Leu Gly Glu Phe His Gln Lys Gly Thr Val Arg	
60 65 70	
ACA AAG TAC GGC ACA AAA GGA GAG CTG CAA TCT GCG ATC AAA AGT CTT	690
Thr Lys Tyr Gly Thr Lys Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu	
75 80 85 90	
CAT TCC CGC GAC ATT AAC GTT TAC GGG GAT GTG GTC ATC AAC CAC AAA	738
His Ser Arg Asp Ile Asn Val Tyr Gly Asp Val Val Ile Asn His Lys	
95 100 105	
GGC GGC GCT GAT GCG ACC GAA GAT GTA ACC GCG GTT GAA GTC GAT CCC	786
Gly Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val Glu Val Asp Pro	
110 115 120	
GCT GAC CGC AAC CGC GTA ATT TCA GGA GAA CAC CTA ATT AAA GCC TGG	834
Ala Asp Arg Asn Arg Val Ile Ser Gly Glu His Leu Ile Lys Ala Trp	
125 130 135	
ACA CAT TTT CAT TTT CCG GGG CGC GGC AGC ACA TAC AGC GAT TTT AAA	882
Thr His Phe His Phe Pro Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys	
140 145 150	
TGG CAT TGG TAC CAT TTT GAC GGA ACC GAT TGG GAC GAG TCC CGA AAG	930
Trp His Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys	
155 160 165 170	
CTG AAC CGC ATC TAT AAG TTT CAA GGA AAG GCT TGG GAT TGG GAA GTT	978
Leu Asn Arg Ile Tyr Lys Phe Gln Gly Lys Ala Trp Asp Trp Glu Val	
175 180 185	
TCC AAT GAA AAC GGC AAC TAT GAT TAT TTG ATG TAT GCC GAC ATC GAT	1026
Ser Asn Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp	
190 195 200	

TAT Tyr	GAC Asp	CAT His 205	CCT Pro	GAT Asp	GTC Val	GCA Ala 210	GCA Ala	GAA Glu	ATT Ile	AAG Lys	AGA Arg 215	TGG Trp	GGC Gly	ACT Thr	TGG Trp	1074
TAT Tyr	GCC Ala 220	AAT Asn	GAA Glu	CTG Leu	CAA Gln 225	TTG Leu	GAC Asp	GGT Gly	TTC Phe	CGT Arg 230	CTT Leu	GAT Asp	GCT Ala	GTC Val	AAA Lys	1122
CAC His 235	ATT Ile	AAA Lys	TTT Phe	TCT Ser 240	TTT Phe	TTG Leu	CGG Arg	GAT Asp	TGG Trp 245	GTT Val	AAT Asn	CAT His	GTC Val	AGG Arg	GAA Glu 250	1170
AAA Lys	ACG Thr	GGG Gly	AAG Lys 255	GAA Glu	ATG Met	TTT Phe	ACG Thr	GTA Val	GCT Ala 260	GAA Glu	TAT Tyr	TGG Trp	CAG Gln	AAT Asn 265	GAC Asp	1218
TTG Leu	GGC Gly	GCG Ala 270	CTG Leu	GAA Glu	AAC Asn	TAT Tyr	TTG Leu	AAC Asn 275	AAA Lys	ACA Thr	AAT Asn	TTT Phe	AAT Asn 280	CAT His	TCA Ser	1266
GTG Val	TTT Phe	GAC Asp 285	GTG Val	CCG Pro	CTT Leu	CAT His 290	TAT Tyr	CAG Gln	TTC Phe	CAT His	GCT Ala 295	GCA Ala	TCG Ser	ACA Thr	CAG Gln	1314
GGA Gly 300	GGC Gly	GGC Gly	TAT Tyr	GAT Asp	ATG Met	AGG Arg 305	AAA Lys	TTG Leu	CTG Leu	AAC Asn	GGT Gly 310	ACG Thr	GTC Val	GTT Val	TCC Ser	1362
AAG Lys 315	CAT His	CCG Pro	TTG Leu	AAA Lys	TCG Ser 320	GTT Val	ACA Thr	TTT Phe	GTC Val	GAT Asp 325	AAC Asn	CAT His	GAT Asp	ACA Thr	CAG Gln 330	1410
CCG Pro	GGG Gly	CAA Gln	TCG Ser 335	CTT Leu	GAG Glu	TCG Ser	ACT Thr	GTC Val	CAA Gln 340	ACA Thr	TGG Trp	TTT Phe	AAG Lys	CCG Pro 345	CTT Leu	1458
GCT Ala	TAC Tyr	GCT Ala 350	TTT Phe	ATT Ile	CTC Leu	ACA Thr	AGG Arg	GAA Glu 355	TCT Ser	GGA Gly	TAC Tyr	CCT Pro	CAG Gln 360	GTT Val	TTC Phe	1506
TAC Tyr	GGG Gly	GAT Asp 365	ATG Met	TAC Tyr	GGG Gly	ACG Thr	AAA Lys 370	GGA Gly	GAC Asp	TCC Ser	CAG Gln 375	CGC Arg	GAA Glu	ATT Ile	CCT Pro	1554
GCC Ala 380	TTG Leu	AAA Lys	CAC His	AAA Lys	ATT Ile	GAA Glu 385	CCG Pro	ATC Ile	TTA Leu	AAA Lys	GCG Ala 390	AGA Arg	AAA Lys	CAG Gln	TAT Tyr	1602
GCG Ala 395	TAC Tyr	GGA Gly	GCA Ala	CAG Gln	CAT His 400	GAT Asp	TAT Tyr	TTC Phe	GAC Asp 405	CAC His	CAT His	GAC Asp	ATT Ile	GTC Val	GGC Gly 410	1650
TGG Trp	ACA Thr	AGG Arg	GAA Glu 415	GGC Gly	GAC Asp	AGC Ser	TCG Ser	GTT Val	GCA Ala 420	AAT Asn	TCA Ser	GGT Gly	TTG Leu	GCG Ala 425	GCA Ala	1698
TTA Leu	ATA Ile	ACA Thr 430	GAC Asp	GGA Gly	CCC Pro	GGT Gly	GGG Gly	GCA Ala 435	AAG Lys	CGA Arg	ATG Met	TAT Tyr	GTC Val 440	GGC Gly	CGG Arg	1746
CAA Gln	AAC Asn 445	GCC Ala	GGT Gly	GAG Glu	ACA Thr	TGG Trp	CAT His 450	GAC Asp	ATT Ile	ACC Thr	GGA Gly 455	AAC Asn	CGT Arg	TCG Ser	GAG Glu	1794
CCG Pro 460	GTT Val	GTC Val	ATC Ile	AAT Asn	TCG Ser	GAA Glu 465	GGC Gly	TGG Trp	GGA Gly	GAG Glu	TTT Phe 470	CAC His	GTA Val	AAC Asn	GGC Gly	1842

GGG TCG GTT TCA ATT TAT GTT CAA AGA TAGAAGAGCA GAGAGGACGG
 Gly Ser Val Ser Ile Tyr Val Gln Arg
 475 480

1889

ATTCCTGAA GGAAATCCGT TTTTATT T

1920

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Gln	Gln	Lys	Arg	Leu	Tyr	Ala	Arg	Leu	Leu	Thr	Leu	Leu	Phe	-29	-25	-20	-15
Ala	Leu	Ile	Phe	Leu	Leu	Pro	His	Ser	Ala	Ala	Ala	Ala	Ala	Asn	Leu	-10	-5	1	
Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Met	Pro	Asn	Asp	Gly	5	10	15	
Gln	His	Trp	Arg	Arg	Leu	Gln	Asn	Asp	Ser	Ala	Tyr	Leu	Ala	Glu	His	20	25	30	35
Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Thr	Ser	Gln	40	45	50	
Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	Phe	55	60	65	
His	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Gly	Glu	Leu	70	75	80	
Gln	Ser	Ala	Ile	Lys	Ser	Leu	His	Ser	Arg	Asp	Ile	Asn	Val	Tyr	Gly	85	90	95	
Asp	Val	Val	Ile	Asn	His	Lys	Gly	Gly	Ala	Asp	Ala	Thr	Glu	Asp	Val	100	105	110	115
Thr	Ala	Val	Glu	Val	Asp	Pro	Ala	Asp	Arg	Asn	Arg	Val	Ile	Ser	Gly	120	125	130	
Glu	His	Leu	Ile	Lys	Ala	Trp	Thr	His	Phe	His	Phe	Pro	Gly	Arg	Gly	135	140	145	
Ser	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	Thr	150	155	160	
Asp	Trp	Asp	Glu	Ser	Arg	Lys	Leu	Asn	Arg	Ile	Tyr	Lys	Phe	Gln	Gly	165	170	175	
Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Asn	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	180	185	190	195
Leu	Met	Tyr	Ala	Asp	Ile	Asp	Tyr	Asp	His	Pro	Asp	Val	Ala	Ala	Glu	200	205	210	
Ile	Lys	Arg	Trp	Gly	Thr	Trp	Tyr	Ala	Asn	Glu	Leu	Gln	Leu	Asp	Gly	215	220	225	

Phe	Arg	Leu	Asp	Ala	Val	Lys	His	Ile	Lys	Phe	Ser	Phe	Leu	Arg	Asp	
		230					235					240				
Trp	Val	Asn	His	Val	Arg	Glu	Lys	Thr	Gly	Lys	Glu	Met	Phe	Thr	Val	
	245					250					255					
Ala	Glu	Tyr	Trp	Gln	Asn	Asp	Leu	Gly	Ala	Leu	Glu	Asn	Tyr	Leu	Asn	
260					265					270					275	
Lys	Thr	Asn	Phe	Asn	His	Ser	Val	Phe	Asp	Val	Pro	Leu	His	Tyr	Gln	
				280					285					290		
Phe	His	Ala	Ala	Ser	Thr	Gln	Gly	Gly	Gly	Tyr	Asp	Met	Arg	Lys	Leu	
			295					300					305			
Leu	Asn	Gly	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ser	Val	Thr	Phe	
	310						315					320				
Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Gln	Ser	Leu	Glu	Ser	Thr	Val	
	325					330					335					
Gln	Thr	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Phe	Ile	Leu	Thr	Arg	Glu	
340					345					350					355	
Ser	Gly	Tyr	Pro	Gln	Val	Phe	Tyr	Gly	Asp	Met	Tyr	Gly	Thr	Lys	Gly	
				360					365					370		
Asp	Ser	Gln	Arg	Glu	Ile	Pro	Ala	Leu	Lys	His	Lys	Ile	Glu	Pro	Ile	
			375					380					385			
Leu	Lys	Ala	Arg	Lys	Gln	Tyr	Ala	Tyr	Gly	Ala	Gln	His	Asp	Tyr	Phe	
		390					395					400				
Asp	His	His	Asp	Ile	Val	Gly	Trp	Thr	Arg	Glu	Gly	Asp	Ser	Ser	Val	
	405					410					415					
Ala	Asn	Ser	Gly	Leu	Ala	Ala	Leu	Ile	Thr	Asp	Gly	Pro	Gly	Gly	Ala	
420					425					430					435	
Lys	Arg	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Glu	Thr	Trp	His	Asp	
				440					445					450		
Ile	Thr	Gly	Asn	Arg	Ser	Glu	Pro	Val	Val	Ile	Asn	Ser	Glu	Gly	Trp	
			455					460					465			
Gly	Glu	Phe	His	Val	Asn	Gly	Gly	Ser	Val	Ser	Ile	Tyr	Val	Gln	Arg	
		470					475					480				

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2084 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 250..1791

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 250..342

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 343..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCCCGCACA TACGAAAAGA CTGGCTGAAA ACATTGAGCC TTTGATGACT GATGATTG	60
CTGAAGAAGT GGATCGATTG TTTGAGAAAA GAAGAAGACC ATAAAAATAC CTTGTCTGTC	120
ATCAGACAGG GTATTTTTTA TGCTGTCCAG ACTGTCCGCT GTGTAAAAAT AAGGAATAAA	180
GGGGGGTTGT TATTATTTTA CTGATATGTA AAATATAATT TGTATAAGAA AATGAGAGGG	240
AGAGGAAAC ATG ATT CAA AAA CGA AAG CGG ACA GTT TCG TTC AGA CTT	288
Met Ile Gln Lys Arg Lys Arg Thr Val Ser Phe Arg Leu	
-31 -30 -25 -20	
GTG CTT ATG TGC ACG CTG TTA TTT GTC AGT TTG CCG ATT ACA AAA ACA	336
Val Leu Met Cys Thr Leu Leu Phe Val Ser Leu Pro Ile Thr Lys Thr	
-15 -10 -5	
TCA GCC GTA AAT GGC ACG CTG ATG CAG TAT TTT GAA TGG TAT ACG CCG	384
Ser Ala Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro	
1 5 10	
AAC GAC GGC CAG CAT TGG AAA CGA TTG CAG AAT GAT GCG GAA CAT TTA	432
Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu	
15 20 25 30	
TCG GAT ATC GGA ATC ACT GCC GTC TGG ATT CCT CCC GCA TAC AAA GGA	480
Ser Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly	
35 40 45	
TTG AGC CAA TCC GAT AAC GGA TAC GGA CCT TAT GAT TTG TAT GAT TTA	528
Leu Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu	
50 55 60	
GGA GAA TTC CAG CAA AAA GGG ACG GTC AGA ACG AAA TAC GGC ACA AAA	576
Gly Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys	
65 70 75	
TCA GAG CTT CAA GAT GCG ATC GGC TCA CTG CAT TCC CGG AAC GTC CAA	624
Ser Glu Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln	
80 85 90	
GTA TAC GGA GAT GTG GTT TTG AAT CAT AAG GCT GGT GCT GAT GCA ACA	672
Val Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr	
95 100 105 110	
GAA GAT GTA ACT GCC GTC GAA GTC AAT CCG GCC AAT AGA AAT CAG GAA	720
Glu Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu	
115 120 125	
ACT TCG GAG GAA TAT CAA ATC AAA GCG TGG ACG GAT TTT CGT TTT CCG	768
Thr Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro	
130 135 140	
GGC CGT GGA AAC ACG TAC AGT GAT TTT AAA TGG CAT TGG TAT CAT TTC	816
Gly Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe	
145 150 155	
GAC GGA GCG GAC TGG GAT GAA TCC CGG AAG ATC AGC CGC ATC TTT AAG	864
Asp Gly Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys	
160 165 170	
TTT CGT GGG GAA GGA AAA GCG TGG GAT TGG GAA GTA TCA AGT GAA AAC	912

Phe 175	Arg	Gly	Glu	Gly	Lys 180	Ala	Trp	Asp	Trp	Glu 185	Val	Ser	Ser	Glu	Asn 190	
GGC Gly	AAC Asn	TAT Tyr	GAC Asp	TAT Tyr 195	TTA Leu	ATG Met	TAT Tyr	GCT Ala	GAT Asp 200	GTT Val	GAC Asp	TAC Tyr	GAC Asp	CAC His 205	CCT Pro	960
GAT Asp	GTC Val	GTG Val	GCA Ala 210	GAG Glu	ACA Thr	AAA Lys	AAA Lys	TGG Trp 215	GGT Gly	ATC Ile	TGG Trp	TAT Tyr	GCG Ala 220	AAT Asn	GAA Glu	1008
CTG Leu	TCA Ser	TTA Leu 225	GAC Asp	GGC Gly	TTC Phe	CGT Arg	ATT Ile 230	GAT Asp	GCC Ala	GCC Ala	AAA Lys	CAT His 235	ATT Ile	AAA Lys	TTT Phe	1056
TCA Ser	TTT Phe 240	CTG Leu	CGT Arg	GAT Asp	TGG Trp	GTT Val 245	CAG Gln	GCG Ala	GTC Val	AGA Arg	CAG Gln 250	GCG Ala	ACG Thr	GGA Gly	AAA Lys	1104
GAA Glu 255	ATG Met	TTT Phe	ACG Thr	GTT Val	GCG Ala 260	GAG Glu	TAT Tyr	TGG Trp	CAG Gln	AAT Asn 265	AAT Asn	GCC Ala	GGG Gly	AAA Lys	CTC Leu 270	1152
GAA Glu	AAC Asn	TAC Tyr	TTG Leu	AAT Asn 275	AAA Lys	ACA Thr	AGC Ser	TTT Phe	AAT Asn 280	CAA Gln	TCC Ser	GTG Val	TTT Phe	GAT Asp 285	GTT Val	1200
CCG Pro	CTT Leu	CAT His	TTC Phe 290	AAT Asn	TTA Leu	CAG Gln	GCG Ala	GCT Ala 295	TCC Ser	TCA Ser	CAA Gln	GGA Gly	GGC Gly 300	GGA Gly	TAT Tyr	1248
GAT Asp	ATG Met	AGG Arg 305	CGT Arg	TTG Leu	CTG Leu	GAC Asp	GGT Gly 310	ACC Thr	GTT Val	GTG Val	TCC Ser	AGG Arg 315	CAT His	CCG Pro	GAA Glu	1296
AAG Lys 320	GCG Ala	GTT Val	ACA Thr	TTT Phe	GTT Val	GAA Glu 325	AAT Asn	CAT His	GAC Asp	ACA Thr	CAG Gln 330	CCG Pro	GGA Gly	CAG Gln	TCA Ser	1344
TTG Leu 335	GAA Glu	TCG Ser	ACA Thr	GTC Val	CAA Gln 340	ACT Thr	TGG Trp	TTT Phe	AAA Lys	CCG Pro 345	CTT Leu	GCA Ala	TAC Tyr	GCC Ala	TTT Phe 350	1392
ATT Ile	TTG Leu	ACA Thr	AGA Arg	GAA Glu 355	TCC Ser	GGT Gly	TAT Tyr	CCT Pro	CAG Gln 360	GTG Val	TTC Phe	TAT Tyr	GGG Gly	GAT Asp 365	ATG Met	1440
TAC Tyr	GGG Gly	ACA Thr	AAA Lys 370	GGG Gly	ACA Thr	TCG Ser	CCA Pro	AAG Lys 375	GAA Glu	ATT Ile	CCC Pro	TCA Ser	CTG Leu 380	AAA Lys	GAT Asp	1488
AAT Asn	ATA Ile	GAG Glu 385	CCG Pro	ATT Ile	TTA Leu	AAA Lys	GCG Ala 390	CGT Arg	AAG Lys	GAG Glu	TAC Tyr	GCA Ala 395	TAC Tyr	GGG Gly	CCC Pro	1536
CAG Gln 400	CAC His	GAT Asp	TAT Tyr	ATT Ile	GAC Asp	CAC His 405	CCG Pro	GAT Asp	GTG Val	ATC Ile	GGA Gly 410	TGG Trp	ACG Thr	AGG Arg	GAA Glu	1584
GGT Gly 415	GAC Asp	AGC Ser	TCC Ser	GCC Ala 420	GCC Ala	AAA Lys	TCA Ser	GGT Gly	TTG Leu	GCC Ala 425	GCT Ala	TTA Leu	ATC Ile	ACG Thr	GAC Asp 430	1632
GGA Gly	CCC Pro	GGC Gly	GGA Gly	TCA Ser 435	AAG Lys	CGG Arg	ATG Met	TAT Tyr	GCC Ala 440	GGC Gly	CTG Leu	AAA Lys	AAT Asn	GCC Ala 445	GGC Gly	1680

GAG ACA TGG TAT GAC ATA ACG GGC AAC CGT TCA GAT ACT GTA AAA ATC	1728
Glu Thr Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile	
450 455 460	
GGA TCT GAC GGC TGG GGA GAG TTT CAT GTA AAC GAT GGG TCC GTC TCC	1776
Gly Ser Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser	
465 470 475	
ATT TAT GTT CAG AAA TAAGGTAATA AAAAAACACC TCCAAGCTGA GTGCGGGTAT	1831
Ile Tyr Val Gln Lys	
480	
CAGCTTGGAG GTGCGTTTAT TTTTTCAGCC GTATGACAAG GTCGGCATCA GGTGTGACAA	1891
ATACGGTATG CTGGCTGTCA TAGGTGACAA ATCCGGGTTT TGCGCCGTTT GGCTTTTTTCA	1951
CATGTCTGAT TTTTGTATAA TCAACAGGCA CGGAGCCGGA ATCTTTCGCC TTGGA AAAAT	2011
AAGCGGCGAT CGTAGCTGCT TCCAATATGG ATTGTTTCATC GGGATCGCTG CTTTTAATCA	2071
CAACGTGGGA TCC	2084

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ile Gln Lys Arg Lys Arg Thr Val Ser Phe Arg Leu Val Leu Met	
-31 -30 -25 -20	
Cys Thr Leu Leu Phe Val Ser Leu Pro Ile Thr Lys Thr Ser Ala Val	
-15 -10 -5 1	
Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly	
5 10 15	
Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile	
20 25 30	
Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln	
35 40 45	
Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe	
50 55 60 65	
Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu	
70 75 80	
Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly	
85 90 95	
Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val	
100 105 110	
Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu	
115 120 125	
Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly	
130 135 140 145	

Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala
 150 155 160
 Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly
 165 170 175
 Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr
 180 185 190
 Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val
 195 200 205
 Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser Leu
 210 215 220 225
 Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe Leu
 230 235 240
 Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe
 245 250 255
 Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn Tyr
 260 265 270
 Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu His
 275 280 285
 Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met Arg
 290 295 300 305
 Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala Val
 310 315 320
 Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser
 325 330 335
 Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr
 340 345 350
 Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr
 355 360 365
 Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile Glu
 370 375 380 385
 Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His Asp
 390 395 400
 Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser
 405 410 415
 Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly
 420 425 430
 Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr Trp
 435 440 445
 Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp
 450 455 460 465
 Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val
 470 475 480
 Gln Lys

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1814 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 156..1802

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 156..257

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 258..1802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
AAATTCGATA TTGAAAACGA TTACAAATAA AAATTATAAT AGACGTAAAC GTTCGAGGGT      60
TTGCTCCCTT TTTACTCTTT TTATGCAATC GTTTCCCTTA ATTTTTTGGG AGCCAAACCG      120
TCGAATGTAA CATTTGATTA AGGGGGAAGG GCATT GTG CTA ACG TTT CAC CGC      173
                               Val Leu Thr Phe His Arg
                               -34                -30

ATC ATT CGA AAA GGA TGG ATG TTC CTG CTC GCG TTT TTG CTC ACT GTC      221
Ile Ile Arg Lys Gly Trp Met Phe Leu Leu Ala Phe Leu Leu Thr Val
                -25                -20                -15

TCG CTG TTC TGC CCA ACA GGA CAG CCC GCC AAG GCT GCC GCA CCG TTT      269
Ser Leu Phe Cys Pro Thr Gly Gln Pro Ala Lys Ala Ala Pro Phe
    -10                -5                1

AAC GGC ACC ATG ATG CAG TAT TTT GAA TGG TAC TTG CCG GAT GAT GGC      317
Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu Pro Asp Asp Gly
    5                10                15                20

ACG TTA TGG ACC AAA GTG GCC AAT GAA GCC AAC AAC TTA TCC AGC CTT      365
Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn Leu Ser Ser Leu
                25                30                35

GGC ATC ACC GCT CTT TGG CTG CCG CCC GCT TAC AAA GGA ACA AGC CGC      413
Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys Gly Thr Ser Arg
                40                45                50

AGC GAC GTA GGG TAC GGA GTA TAC GAC TTG TAT GAC CTC GGC GAA TTC      461
Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
    55                60                65

AAT CAA AAA GGG ACC GTC CGC ACA AAA TAC GGA ACA AAA GCT CAA TAT      509
Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln Tyr
    70                75                80

CTT CAA GCC ATT CAA GCC GCC CAC GCC GCT GGA ATG CAA GTG TAC GCC      557
Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met Gln Val Tyr Ala
    85                90                95                100

GAT GTC GTG TTC GAC CAT AAA GGC GGC GCT GAC GGC ACG GAA TGG GTG      605
Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly Thr Glu Trp Val
                105                110                115
```

GAC Asp	GCC Ala	GTC Val	GAA Glu 120	GTC Val	AAT Asn	CCG Pro	TCC Ser	GAC Asp 125	CGC Arg	AAC Asn	CAA Gln	GAA Glu	ATC Ile 130	TCG Ser	GGC Gly	653
ACC Thr	TAT Tyr	CAA Gln 135	ATC Ile	CAA Gln	GCA Ala	TGG Trp	ACG Thr 140	AAA Lys	TTT Phe	GAT Asp	TTT Phe	CCC Pro 145	GGG Gly	CGG Arg	GGC Gly	701
AAC Asn 150	ACC Thr	TAC Tyr	TCC Ser	AGC Ser	TTT Phe	AAG Lys 155	TGG Trp	CGC Arg	TGG Trp	TAC Tyr	CAT His 160	TTT Phe	GAC Asp	GGC Gly	GTT Val	749
GAT Asp 165	TGG Trp	GAC Asp	GAA Glu	AGC Ser	CGA Arg 170	AAA Lys	TTG Leu	AGC Ser	CGC Arg	ATT Ile 175	TAC Tyr	AAA Lys	TTC Phe	CGC Arg	GGC Gly 180	797
ATC Ile	GGC Gly	AAA Lys	GCG Ala	TGG Trp 185	GAT Asp	TGG Trp	GAA Glu	GTA Val	GAC Asp 190	ACG Thr	GAA Glu	AAC Asn	GGA Gly	AAC Asn 195	TAT Tyr	845
GAC Asp	TAC Tyr	TTA Leu 200	ATG Met	TAT Tyr	GCC Ala	GAC Asp	CTT Leu 205	GAT Asp	ATG Met	GAT Asp	CAT His	CCC Pro 210	GAA Glu	GTC Val	GTG Val	893
ACC Thr	GAG Glu	CTG Leu 215	AAA Lys	AAC Asn	TGG Trp	GGG Gly	AAA Lys 220	TGG Trp	TAT Tyr	GTC Val	AAC Asn	ACA Thr 225	ACG Thr	AAC Asn	ATT Ile	941
GAT Asp 230	GGG Gly	TTC Phe	CGG Arg	CTT Leu	GAT Asp	GCC Ala 235	GTC Val	AAG Lys	CAT His	ATT Ile	AAG Lys 240	TTC Phe	AGT Ser	TTT Phe	TTT Phe	989
CCT Pro 245	GAT Asp	TGG Trp	TTG Leu	TCG Ser	TAT Tyr 250	GTG Val	CGT Arg	TCT Ser	CAG Gln	ACT Thr 255	GGC Gly	AAG Lys	CCG Pro	CTA Leu	TTT Phe 260	1037
ACC Thr	GTC Val	GGG Gly	GAA Glu	TAT Tyr 265	TGG Trp	AGC Ser	TAT Tyr	GAC Asp	ATC Ile 270	AAC Asn	AAG Lys	TTG Leu	CAC His	AAT Asn 275	TAC Tyr	1085
ATT Ile	ACG Thr	AAA Lys 280	ACA Thr	GAC Asp	GGA Gly	ACG Thr	ATG Met	TCT Ser 285	TTG Leu	TTT Phe	GAT Asp	GCC Ala 290	CCG Pro	TTA Leu	CAC His	1133
AAC Asn	AAA Lys 295	TTT Phe	TAT Tyr	ACC Thr	GCT Ala	TCC Ser	AAA Lys 300	TCA Ser	GGG Gly	GGC Gly	GCA Ala 305	TTT Phe	GAT Asp	ATG Met	CGC Arg	1181
ACG Thr 310	TTA Leu	ATG Met	ACC Thr	AAT Asn	ACT Thr	CTC Leu 315	ATG Met	AAA Lys	GAT Asp	CAA Gln	CCG Pro 320	ACA Thr	TTG Leu	GCC Ala	GTC Val	1229
ACC Thr 325	TTC Phe	GTT Val	GAT Asp	AAT Asn	CAT His 330	GAC Asp	ACC Thr	GAA Glu	CCC Pro	GGC Gly 335	CAA Gln	GCG Ala	CTG Leu	CAG Gln	TCA Ser 340	1277
TGG Trp	GTC Val	GAC Asp	CCA Pro	TGG Trp 345	TTC Phe	AAA Lys	CCG Pro	TTG Leu	GCT Ala 350	TAC Tyr	GCC Ala	TTT Phe	ATT Ile	CTA Leu 355	ACT Thr	1325
CGG Arg	CAG Gln	GAA Glu	GGA Gly 360	TAC Tyr	CCG Pro	TGC Cys	GTC Val	TTT Phe 365	TAT Tyr	GGT Gly	GAC Asp	TAT Tyr	TAT Tyr 370	GGC Gly	ATT Ile	1373

CCA CAA TAT AAC ATT CCT TCG CTG AAA AGC AAA ATC GAT CCG CTC CTC	1421
Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu	
375 380 385	
ATC GCG CGC AGG GAT TAT GCT TAC GGA ACG CAA CAT GAT TAT CTT GAT	1469
Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp	
390 395 400	
CAC TCC GAC ATC ATC GGG TGG ACA AGG GAA GGG GGC ACT GAA AAA CCA	1517
His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Thr Glu Lys Pro	
405 410 415 420	
GGA TCC GGA CTG GCC GCA CTG ATC ACC GAT GGG CCG GGA GGA AGC AAA	1565
Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys	
425 430 435	
TGG ATG TAC GTT GGC AAA CAA CAC GCT GGA AAA GTG TTC TAT GAC CTT	1613
Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val Phe Tyr Asp Leu	
440 445 450	
ACC GGC AAC CGG AGT GAC ACC GTC ACC ATC AAC AGT GAT GGA TGG GGG	1661
Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser Asp Gly Trp Gly	
455 460 465	
GAA TTC AAA GTC AAT GGC GGT TCG GTT TCG GTT TGG GTT CCT AGA AAA	1709
Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp Val Pro Arg Lys	
470 475 480	
ACG ACC GTT TCT ACC ATC GCT CGG CCG ATC ACA ACC CGA CCG TGG ACT	1757
Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr Arg Pro Trp Thr	
485 490 495 500	
GGT GAA TTC GTC CGT TGG ACC GAA CCA CGG TTG GTG GCA TGG CCT	1802
Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val Ala Trp Pro	
505 510 515	
TGATGCCTGC GA	1814

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 549 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu	
-34 -30 -25 -20	
Ala Phe Leu Leu Thr Val Ser Leu Phe Cys Pro Thr Gly Gln Pro Ala	
-15 -10 -5	
Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp	
1 5 10	
Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala	
15 20 25 30	
Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala	
35 40 45	
Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu	
50 55 60	

Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr
65 70 75
Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala
80 85 90
Gly Met Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala
95 100 105 110
Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg
115 120 125
Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
130 135 140
Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
145 150 155
Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg
160 165 170
Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp
175 180 185 190
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met
195 200 205
Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr
210 215 220
Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His
225 230 235
Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln
240 245 250
Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile
255 260 265 270
Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu
275 280 285
Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly
290 295 300
Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp
305 310 315
Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro
320 325 330
Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala
335 340 345 350
Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr
355 360 365
Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser
370 375 380
Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr
385 390 395
Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu
400 405 410

Gly Gly Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp
 415 420 425 430
 Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly
 435 440 445
 Lys Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile
 450 455 460
 Asn Ser Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser
 465 470 475
 Val Trp Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile
 480 485 490
 Thr Thr Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg
 495 500 505 510
 Leu Val Ala Trp Pro
 515

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGTCGTAGGC ACCGTAGCCC CAATCCGCTT G

31

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTCGTAGGC ACCGTAGCCC CAATCCCATT GGCTCG

36

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGTGACTGG TGAGTACTCA ACCAAGTC

28

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala	Thr	Pro	Ala	Asp	Trp	Arg	Ser	Gln	Ser	Ile	Tyr	Phe	Leu	Leu	Thr	
1				5					10					15		
Asp	Arg	Phe	Ala	Arg	Thr	Asp	Gly	Ser	Thr	Thr	Ala	Thr	Cys	Asn	Thr	
			20					25					30			
Ala	Asp	Gln	Lys	Tyr	Cys	Gly	Gly	Thr	Trp	Gln	Gly	Ile	Ile	Asp	Lys	
			35				40					45				
Leu	Asp	Tyr	Ile	Gln	Gly	Met	Gly	Phe	Thr	Ala	Ile	Trp	Ile	Thr	Pro	
	50					55					60					
Val	Thr	Ala	Gln	Leu	Pro	Gln	Thr	Thr	Ala	Tyr	Gly	Asp	Ala	Tyr	His	
65					70					75					80	
Gly	Tyr	Trp	Gln	Gln	Asp	Ile	Tyr	Ser	Leu	Asn	Glu	Asn	Tyr	Gly	Thr	
				85					90					95		
Ala	Asp	Asp	Leu	Lys	Ala	Leu	Ser	Ser	Ala	Leu	His	Glu	Arg	Gly	Met	
			100					105					110			
Tyr	Leu	Met	Val	Asp	Val	Val	Ala	Asn	His	Met	Gly	Tyr	Asp	Gly	Ala	
		115					120					125				
Gly	Ser	Ser	Val	Asp	Tyr	Ser	Val	Phe	Lys	Pro	Phe	Ser	Ser	Gln	Asp	
	130					135					140					
Tyr	Phe	His	Pro	Phe	Cys	Phe	Ile	Gln	Asn	Tyr	Glu	Asp	Gln	Thr	Gln	
145					150					155					160	
Val	Glu	Asp	Cys	Trp	Leu	Gly	Asp	Asn	Thr	Val	Ser	Leu	Pro	Asp	Leu	
				165					170					175		
Asp	Thr	Thr	Lys	Asp	Val	Val	Lys	Asn	Glu	Trp	Tyr	Asp	Trp	Val	Gly	
			180					185					190			
Ser	Leu	Val	Ser	Asn	Tyr	Ser	Ile	Asp	Gly	Leu	Arg	Ile	Asp	Thr	Val	
		195					200					205				
Lys	His	Val	Gln	Lys	Asp	Phe	Trp	Pro	Gly	Tyr	Asn	Lys	Ala	Ala	Gly	
	210					215					220					
Val	Tyr	Cys	Ile	Gly	Glu	Val	Leu	Asp	Gly	Asp	Pro	Ala	Tyr	Thr	Cys	
225					230					235					240	
Pro	Tyr	Gln	Asn	Val	Met	Asp	Gly	Val	Leu	Asn	Tyr	Pro	Ile	Tyr	Tyr	
				245					250					255		
Pro	Leu	Leu	Asn	Ala	Phe	Lys	Ser	Thr	Ser	Gly	Ser	Met	Asp	Asp	Leu	
			260					265					270			
Tyr	Asn	Met	Ile	Asn	Thr	Val	Lys	Ser	Asp	Cys	Pro	Asp	Ser	Thr	Leu	
		275					280					285				

Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
 290 295 300
 Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
 305 310 315 320
 Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
 325 330 335
 Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
 340 345 350
 Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala Asn Ala Ile
 355 360 365
 Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
 370 375 380
 Trp Pro Ile Tyr Lys Asp Asp Ile Thr Ile Ala Met Arg Lys Gly Thr
 385 390 395 400
 Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
 405 410 415
 Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
 420 425 430
 Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
 435 440 445
 Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
 450 455 460
 Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser
 465 470 475

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CAT CAT AAT GGA ACA AAT GGT ACT ATG ATG CAA TAT TTC GAA TGG TAT	48
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr	
520 525 530	
TTG CCA AAT GAC GGG AAT CAT TGG AAC AGG TTG AGG GAT GAC GCA GCT	96
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala	
535 540 545	
AAC TTA AAG AGT AAA GGG ATA ACA GCT GTA TGG ATC CCA CCT GCA TGG	144
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp	
550 555 560	
AAG GGG ACT TCC CAG AAT GAT GTA GGT TAT GGA GCC TAT GAT TTA TAT	192
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr	

565						570						575						
GAT	CTT	GGA	GAG	TTT	AAC	CAG	AAG	GGG	ACG	GTT	CGT	ACA	AAA	TAT	GGA			240
Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly			
580					585					590					595			
ACA	CGC	AAC	CAG	CTA	CAG	GCT	GCG	GTG	ACC	TCT	TTA	AAA	AAT	AAC	GGC			288
Thr	Arg	Asn	Gln	Leu	Gln	Ala	Ala	Val	Thr	Ser	Leu	Lys	Asn	Asn	Gly			
				600					605					610				
ATT	CAG	GTA	TAT	GGT	GAT	GTC	GTC	ATG	AAT	CAT	AAA	GGT	GGA	GCA	GAT			336
Ile	Gln	Val	Tyr	Gly	Asp	Val	Val	Met	Asn	His	Lys	Gly	Gly	Ala	Asp			
			615					620					625					
GGT	ACG	GAA	ATT	GTA	AAT	GCG	GTA	GAA	GTG	AAT	CGG	AGC	AAC	CGA	AAC			384
Gly	Thr	Glu	Ile	Val	Asn	Ala	Val	Glu	Val	Asn	Arg	Ser	Asn	Arg	Asn			
		630					635					640						
CAG	GAA	ACC	TCA	GGA	GAG	TAT	GCA	ATA	GAA	GCG	TGG	ACA	AAG	TTT	GAT			432
Gln	Glu	Thr	Ser	Gly	Glu	Tyr	Ala	Ile	Glu	Ala	Trp	Thr	Lys	Phe	Asp			
	645					650					655							
TTT	CCT	GGA	AGA	GGA	AAT	AAC	CAT	TCC	AGC	TTT	AAG	TGG	CGC	TGG	TAT			480
Phe	Pro	Gly	Arg	Gly	Asn	Asn	His	Ser	Ser	Phe	Lys	Trp	Arg	Trp	Tyr			
660					665					670					675			
CAT	TTT	GAT	GGG	ACA	GAT	TGG	GAT	CAG	TCA	CGC	CAG	CTT	CAA	AAC	AAA			528
His	Phe	Asp	Gly	Thr	Asp	Trp	Asp	Gln	Ser	Arg	Gln	Leu	Gln	Asn	Lys			
				680				685						690				
ATA	TAT	AAA	TTC	AGG	GGA	ACA	GGC	AAG	GCC	TGG	GAC	TGG	GAA	GTC	GAT			576
Ile	Tyr	Lys	Phe	Arg	Gly	Thr	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Asp			
			695					700					705					
ACA	GAG	AAT	GGC	AAC	TAT	GAC	TAT	CTT	ATG	TAT	GCA	GAC	GTG	GAT	ATG			624
Thr	Glu	Asn	Gly	Asn	Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Met			
		710				715					720							
GAT	CAC	CCA	GAA	GTA	ATA	CAT	GAA	CTT	AGA	AAC	TGG	GGA	GTG	TGG	TAT			672
Asp	His	Pro	Glu	Val	Ile	His	Glu	Leu	Arg	Asn	Trp	Gly	Val	Trp	Tyr			
	725				730						735							
ACG	AAT	ACA	CTG	AAC	CTT	GAT	GGA	TTT	AGA	ATA	GAT	GCA	GTG	AAA	CAT			720
Thr	Asn	Thr	Leu	Asn	Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Val	Lys	His			
740				745					750					755				
ATA	AAA	TAT	AGC	TTT	ACG	AGA	GAT	TGG	CTT	ACA	CAT	GTG	CGT	AAC	ACC			768
Ile	Lys	Tyr	Ser	Phe	Thr	Arg	Asp	Trp	Leu	Thr	His	Val	Arg	Asn	Thr			
			760					765						770				
ACA	GGT	AAA	CCA	ATG	TTT	GCA	GTG	GCT	GAG	TTT	TGG	AAA	AAT	GAC	CTT			816
Thr	Gly	Lys	Pro	Met	Phe	Ala	Val	Ala	Glu	Phe	Trp	Lys	Asn	Asp	Leu			
			775				780						785					
GGT	GCA	ATT	GAA	AAC	TAT	TTG	AAT	AAA	ACA	AGT	TGG	AAT	CAC	TCG	GTG			864
Gly	Ala	Ile	Glu	Asn	Tyr	Leu	Asn	Lys	Thr	Ser	Trp	Asn	His	Ser	Val			
		790					795					800						
TTT	GAT	GTT	CCT	CTC	CAC	TAT	AAT	TTG	TAC	AAT	GCA	TCT	AAT	AGC	GGT			912
Phe	Asp	Val	Pro	Leu	His	Tyr	Asn	Leu	Tyr	Asn	Ala	Ser	Asn	Ser	Gly			
	805					810					815							
GGT	TAT	TAT	GAT	ATG	AGA	AAT	ATT	TTA	AAT	GGT	TCT	GTG	GTG	CAA	AAA			960
Gly	Tyr	Tyr	Asp	Met	Arg	Asn	Ile	Leu	Asn	Gly	Ser	Val	Val	Gln	Lys			
820				825					830					835				
CAT	CCA	ACA	CAT	GCC	GTT	ACT	TTT	GTT	GAT	AAC	CAT	GAT	TCT	CAG	CCC			1008

His	Pro	Thr	His	Ala	Val	Thr	Phe	Val	Asp	Asn	His	Asp	Ser	Gln	Pro		
				840					845					850			
GGG	GAA	GCA	TTG	GAA	TCC	TTT	GTT	CAA	CAA	TGG	TTT	AAA	CCA	CTT	GCA		1056
Gly	Glu	Ala	Leu	Glu	Ser	Phe	Val	Gln	Gln	Trp	Phe	Lys	Pro	Leu	Ala		
			855					860					865				
TAT	GCA	TTG	GTT	CTG	ACA	AGG	GAA	CAA	GGT	TAT	CCT	TCC	GTA	TTT	TAT		1104
Tyr	Ala	Leu	Val	Leu	Thr	Arg	Gln	Gly	Tyr	Pro	Ser	Val	Phe	Tyr			
			870				875					880					
GGG	GAT	TAC	TAC	GGT	ATC	CCA	ACC	CAT	GGT	GTT	CCG	GCT	ATG	AAA	TCT		1152
Gly	Asp	Tyr	Tyr	Gly	Ile	Pro	Thr	His	Gly	Val	Pro	Ala	Met	Lys	Ser		
	885					890					895						
AAA	ATA	GAC	CCT	CTT	CTG	CAG	GCA	CGT	CAA	ACT	TTT	GCC	TAT	GGT	ACG		1200
Lys	Ile	Asp	Pro	Leu	Leu	Gln	Ala	Arg	Gln	Thr	Phe	Ala	Tyr	Gly	Thr		
	900				905					910					915		
CAG	CAT	GAT	TAC	TTT	GAT	CAT	CAT	GAT	ATT	ATC	GGT	TGG	ACA	AGA	GAG		1248
Gln	His	Asp	Tyr	Phe	Asp	His	His	Asp	Ile	Ile	Gly	Trp	Thr	Arg	Glu		
				920					925					930			
GGA	AAT	AGC	TCC	CAT	CCA	AAT	TCA	GGC	CTT	GCC	ACC	ATT	ATG	TCA	GAT		1296
Gly	Asn	Ser	Ser	His	Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asp		
			935					940					945				
GGT	CCA	GGT	GGT	AAC	AAA	TGG	ATG	TAT	GTG	GGG	AAA	AAT	AAA	GCG	GGA		1344
Gly	Pro	Gly	Gly	Asn	Lys	Trp	Met	Tyr	Val	Gly	Lys	Asn	Lys	Ala	Gly		
			950				955					960					
CAA	GTT	TGG	AGA	GAT	ATT	ACC	GGA	AAT	AGG	ACA	GGC	ACC	GTC	ACA	ATT		1392
Gln	Val	Trp	Arg	Asp	Ile	Thr	Gly	Asn	Arg	Thr	Gly	Thr	Val	Thr	Ile		
			965			970					975						
AAT	GCA	GAC	GGA	TGG	GGT	AAT	TTC	TCT	GTT	AAT	GGA	GGG	TCC	GTT	TCG		1440
Asn	Ala	Asp	Gly	Trp	Gly	Asn	Phe	Ser	Val	Asn	Gly	Gly	Ser	Val	Ser		
					985					990					995		
GTT	TGG	GTG	AAG	CAA	TAA												1458
Val	Trp	Val	Lys	Gln													
				1000													

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

His	His	Asn	Gly	Thr	Asn	Gly	Thr	Met	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	
1				5					10					15		
Leu	Pro	Asn	Asp	Gly	Asn	His	Trp	Asn	Arg	Leu	Arg	Asp	Asp	Ala	Ala	
			20					25					30			
Asn	Leu	Lys	Ser	Lys	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Trp	
			35				40					45				
Lys	Gly	Thr	Ser	Gln	Asn	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	
	50					55					60					

Asp 65	Leu	Gly	Glu	Phe	Asn 70	Gln	Lys	Gly	Thr	Val 75	Arg	Thr	Lys	Tyr	Gly 80
Thr	Arg	Asn	Gln	Leu 85	Gln	Ala	Ala	Val	Thr 90	Ser	Leu	Lys	Asn	Asn 95	Gly
Ile	Gln	Val	Tyr 100	Gly	Asp	Val	Val	Met 105	Asn	His	Lys	Gly	Gly 110	Ala	Asp
Gly	Thr	Glu 115	Ile	Val	Asn	Ala	Val 120	Glu	Val	Asn	Arg	Ser	Asn 125	Arg	Asn
Gln	Glu 130	Thr	Ser	Gly	Glu	Tyr 135	Ala	Ile	Glu	Ala	Trp 140	Thr	Lys	Phe	Asp
Phe 145	Pro	Gly	Arg	Gly	Asn 150	Asn	His	Ser	Ser	Phe 155	Lys	Trp	Arg	Trp	Tyr 160
His	Phe	Asp	Gly	Thr 165	Asp	Trp	Asp	Gln	Ser 170	Arg	Gln	Leu	Gln	Asn 175	Lys
Ile	Tyr	Lys	Phe 180	Arg	Gly	Thr	Gly	Lys 185	Ala	Trp	Asp	Trp	Glu 190	Val	Asp
Thr	Glu	Asn 195	Gly	Asn	Tyr	Asp	Tyr 200	Leu	Met	Tyr	Ala	Asp 205	Val	Asp	Met
Asp 210	His	Pro	Glu	Val	Ile	His 215	Glu	Leu	Arg	Asn	Trp 220	Gly	Val	Trp	Tyr
Thr 225	Asn	Thr	Leu	Asn	Leu 230	Asp	Gly	Phe	Arg	Ile 235	Asp	Ala	Val	Lys	His 240
Ile	Lys	Tyr	Ser	Phe 245	Thr	Arg	Asp	Trp	Leu 250	Thr	His	Val	Arg	Asn 255	Thr
Thr	Gly	Lys	Pro 260	Met	Phe	Ala	Val	Ala 265	Glu	Phe	Trp	Lys	Asn 270	Asp	Leu
Gly	Ala	Ile 275	Glu	Asn	Tyr	Leu	Asn 280	Lys	Thr	Ser	Trp	Asn 285	His	Ser	Val
Phe 290	Asp	Val	Pro	Leu	His	Tyr 295	Asn	Leu	Tyr	Asn	Ala 300	Ser	Asn	Ser	Gly
Gly 305	Tyr	Tyr	Asp	Met	Arg 310	Asn	Ile	Leu	Asn	Gly 315	Ser	Val	Val	Gln	Lys 320
His	Pro	Thr	His	Ala 325	Val	Thr	Phe	Val	Asp 330	Asn	His	Asp	Ser	Gln 335	Pro
Gly	Glu	Ala	Leu 340	Glu	Ser	Phe	Val	Gln 345	Gln	Trp	Phe	Lys	Pro 350	Leu	Ala
Tyr	Ala	Leu 355	Val	Leu	Thr	Arg	Glu 360	Gln	Gly	Tyr	Pro	Ser 365	Val	Phe	Tyr
Gly 370	Asp	Tyr	Tyr	Gly	Ile	Pro 375	Thr	His	Gly	Val	Pro 380	Ala	Met	Lys	Ser
Lys 385	Ile	Asp	Pro	Leu	Leu 390	Gln	Ala	Arg	Gln	Thr 395	Phe	Ala	Tyr	Gly	Thr 400
Gln	His	Asp	Tyr	Phe 405	Asp	His	His	Asp	Ile 410	Ile	Gly	Trp	Thr	Arg 415	Glu

Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
435 440 445

Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Val Trp Val Lys Gln
485

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Val	Asn	Gly	Thr	Leu	Met	Gln	Tyr	Phe	Glu	Trp	Tyr	Thr	Pro	Asn	Asp	1	5	10	15
Gly	Gln	His	Trp	Lys	Arg	Leu	Gln	Asn	Asp	Ala	Glu	His	Leu	Ser	Asp	20	25	30	
Ile	Gly	Ile	Thr	Ala	Val	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	Leu	Ser	35	40	45	
Gln	Ser	Asp	Asn	Gly	Tyr	Gly	Pro	Tyr	Asp	Leu	Tyr	Asp	Leu	Gly	Glu	50	55	60	
Phe	Gln	Gln	Lys	Gly	Thr	Val	Arg	Thr	Lys	Tyr	Gly	Thr	Lys	Ser	Glu	65	70	75	80
Leu	Gln	Asp	Ala	Ile	Gly	Ser	Leu	His	Ser	Arg	Asn	Val	Gln	Val	Tyr	85	90	95	
Gly	Asp	Val	Val	Leu	Asn	His	Lys	Ala	Gly	Ala	Asp	Ala	Thr	Glu	Asp	100	105	110	
Val	Thr	Ala	Val	Glu	Val	Asn	Pro	Ala	Asn	Arg	Asn	Gln	Glu	Thr	Ser	115	120	125	
Glu	Glu	Tyr	Gln	Ile	Lys	Ala	Trp	Thr	Asp	Phe	Arg	Phe	Pro	Gly	Arg	130	135	140	
Gly	Asn	Thr	Tyr	Ser	Asp	Phe	Lys	Trp	His	Trp	Tyr	His	Phe	Asp	Gly	145	150	155	160
Ala	Asp	Trp	Asp	Glu	Ser	Arg	Lys	Ile	Ser	Arg	Ile	Phe	Lys	Phe	Arg	165	170	175	
Gly	Glu	Gly	Lys	Ala	Trp	Asp	Trp	Glu	Val	Ser	Ser	Glu	Asn	Gly	Asn	180	185	190	
Tyr	Asp	Tyr	Leu	Met	Tyr	Ala	Asp	Val	Asp	Tyr	Asp	His	Pro	Asp	Val	195	200	205	
Val	Ala	Glu	Thr	Lys	Lys	Trp	Gly	Ile	Trp	Tyr	Ala	Asn	Glu	Leu	Ser	210	215	220	
Leu	Asp	Gly	Phe	Arg	Ile	Asp	Ala	Ala	Lys	His	Ile	Lys	Phe	Ser	Phe	225	230	235	240
Leu	Arg	Asp	Trp	Val	Gln	Ala	Val	Arg	Gln	Ala	Thr	Gly	Lys	Glu	Met	245	250	255	
Phe	Thr	Val	Ala	Glu	Tyr	Trp	Gln	Asn	Ala	Gly	Lys	Leu	Glu	Asn		260	265	270	
Tyr	Leu	Asn	Lys	Thr	Ser	Phe	Asn	Gln	Ser	Val	Phe	Asp	Val	Pro	Leu	275	280	285	
His	Phe	Asn	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Gly	Gly	Gly	Tyr	Asp	Met	290	295	300	
Arg	Lys	Leu	Leu	Asn	Gly	Thr	Val	Val	Ser	Lys	His	Pro	Leu	Lys	Ser	305	310	315	320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
 435 440 445
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 Val Gln Arg